SEQUENCE LISTING

<110> Green, Allan
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      Lenman, Marit
      Stymne, Sten

<120> FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN
MODIFYING FATTY ACID METABOLISM

<130> 26-98A

<150> US 09/059769

<151> 1998-04-14

<150> US 60/043706

<151> 1997-04-16

<150> AU PO6223

<151> 1997-04-15

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<151> 1997-04-15

<150> US 60/050403

<151> 1997-06-20

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 1358

<212> DNA

<213> Crepis palaestina

<220>

<221> CDS

<222> (30)..(1151)

<223>

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                                  Met Gly Ala Gly Gly Arg Gly Arg
                                  1               5

aca tcg gaa aaa tcg gtc atg gaa cgt gtc tca gtt gat cca gta acc        101
Thr Ser Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr
    10              15                  20

ttc tca ctg agt gaa ttg aag caa gca atc cct ccc cat tgc ttc cag        149
Phe Ser Leu Ser Glu Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln
25                  30                  35                  40

aga tct gta atc cgc tca tct tac tat gtt gtt caa gat ctc att att        197
Arg Ser Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile
                45                  50                  55

gcc tac atc ttc tac ttc ctt gcc aac aca tat atc cct act ctt cct        245
Ala Tyr Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Thr Leu Pro
                60                  65                  70

act agt cta gcc tac tta gct tgg ccc gtt tac tgg ttc tgt caa gct        293
Thr Ser Leu Ala Tyr Leu Ala Trp Pro Val Tyr Trp Phe Cys Gln Ala
            75                  80                  85

agc gtc ctc act ggc tta tgg atc ctc ggc cac gaa tgt ggt cac cat        341
Ser Val Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His
        90                  95                  100

gcc ttt agc aac tac aca tgg ttt gac gac act gtg ggc ttc atc ctc        389
Ala Phe Ser Asn Tyr Thr Trp Phe Asp Asp Thr Val Gly Phe Ile Leu
105                 110                 115                 120

cac tca ttt ctc ctc acc ccg tat ttc tct tgg aaa ttc agt cac cgg        437
His Ser Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Phe Ser His Arg
                125                 130                 135
```

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aat cac cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att      485
Asn His His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile
            140             145             150

ccg aaa agc aag tcc aaa ctc gcg cgt atc tat aaa ctt ctt aac aac      533
Pro Lys Ser Lys Ser Lys Leu Ala Arg Ile Tyr Lys Leu Leu Asn Asn
            155             160             165

cca cct ggt cgg ctg ttg gtt ttg att atc atg ttc acc cta gga ttt      581
Pro Pro Gly Arg Leu Leu Val Leu Ile Ile Met Phe Thr Leu Gly Phe
170             175             180

cct tta tac ctc ttg aca aat att tcc ggc aag aaa tac gac agg ttt      629
Pro Leu Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe
185             190             195             200

gcc aac cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg      677
Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg
            205             210             215

ttt cag gtc ttc ctt tcg gat ctt ggt ctt ctt gcc gtg ttt tat gga      725
Phe Gln Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly
            220             225             230

att aaa gtt gct gta gca aat aaa gga gct gct tgg gta gcg tgc atg      773
Ile Lys Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met
            235             240             245

tat gga gtt ccg gta tta ggc gta ttt acc ttt ttc gat gtg atc acc      821
Tyr Gly Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr
            250             255             260

ttc ttg cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa      869
Phe Leu His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu
265             270             275             280

tgg aac tgg atc aga ggg gcc ttg tca gca atc gat agg gac ttt gga      917
Trp Asn Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Arg Asp Phe Gly
            285             290             295

ttc ctg aat agt gtt ttc cat gat gtt aca cac act cat gtc atg cat      965
Phe Leu Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His
            300             305             310

cat ttg ttt tca tac att cca cac tat cat gca aag gag gca agg gat     1013
His Leu Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp
            315             320             325

gca atc aag cca atc ttg ggc gac ttt tat atg atc gac agg act cca     1061
Ala Ile Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro
            330             335             340

att tta aaa gca atg tgg aga gag ggc agg gag tgc atg tac atc gag     1109
Ile Leu Lys Ala Met Trp Arg Glu Gly Arg Glu Cys Met Tyr Ile Glu
345             350             355             360
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```
cct gat agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg          1151
Pro Asp Ser Lys Leu Lys Gly Val Tyr Trp Tyr His Lys Leu
            365                 370

tgatcatatg caaaatgcac atgcattttc aaaccctcta gttacgtttg ttctatgtat   1211

aataaaccgc cggtcctttg gttgactatg cctaagccag gcgaaacagt taaataatat   1271

cggtatgatg tgtaatgaaa gtatgtggtt gtctggtttt gttgctatga agaaagtat    1331

gtggttgtcg gtcaaaaaaa aaaaaaa                                       1358
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<210> 2

<211> 374

<212> PRT

<213> Crepis palaestina

<400> 2

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Met Gly Ala Gly Gly Arg Gly Arg Thr Ser Glu Lys Ser Val Met Glu
1               5                   10                  15


Arg Val Ser Val Asp Pro Val Thr Phe Ser Leu Ser Glu Leu Lys Gln
            20                  25                  30


Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr
            35                  40                  45


Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala
    50                  55                  60


Asn Thr Tyr Ile Pro Thr Leu Pro Thr Ser Leu Ala Tyr Leu Ala Trp
65                  70                  75                  80


Pro Val Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile
                85                  90                  95


Leu Gly His Glu Cys Gly His His Ala Phe Ser Asn Tyr Thr Trp Phe
                100                 105                 110


Asp Asp Thr Val Gly Phe Ile Leu His Ser Phe Leu Leu Thr Pro Tyr
            115                 120                 125
```

Phe Ser Trp Lys Phe Ser His Arg Asn His His Ser Asn Thr Ser Ser
    130   135   140

Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala
145   150   155   160

Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu
            165   170   175

Ile Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile
        180   185   190

Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser
        195   200   205

Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu
    210   215   220

Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys
225   230   235   240

Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val
            245   250   255

Phe Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser
        260   265   270

Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu
        275   280   285

Ser Ala Ile Asp Arg Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp
    290   295   300

Val Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His
305   310   315   320

Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp
            325   330   335

Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu
        340   345   350

```
Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val
        355                 360                 365

Tyr Trp Tyr His Lys Leu
    370
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<210> 3

<211> 1309

<212> DNA

<213> Crepis sp.

<220>

<221> misc_feature

<222> (937)..(937)

<223> N is any nucleotide residue

<220>

<221> CDS

<222> (26)..(1147)

<223>

<220>

<221> misc_feature

<222> (901)..(901)

<223> N is any nucleotide residue


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tgttgaccat aaatcatcta tcaac atg ggt gcc ggc ggc cgt ggt cgg tcg         52
                             Met Gly Ala Gly Gly Arg Gly Arg Ser
                             1               5

gaa aag tcg gtc atg gaa cgt gtc tca gtt gat cca gta acc ttc tca        100
Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr Phe Ser
10              15              20              25

ctg agt gat ttg aag caa gca atc cct cca cat tgc ttc cag cga tct        148
Leu Ser Asp Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln Arg Ser
            30              35              40
```

```
gtc atc cgt tca tct tat tac gtt gtt cag gat ctc ata att gcc tac        196
Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr
            45                  50                  55

atc ttc tac ttc ctt gcc aac aca tat atc cct aat ctc cct cat cct        244
Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Asn Leu Pro His Pro
        60                  65                  70

cta gcc tac tta gct tgg ccg ctt tac tgg ttc tgt caa gct agc gtc        292
Leu Ala Tyr Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Ala Ser Val
        75                  80                  85

ctc act ggg tta tgg atc ctc ggc cat gaa tgt ggt cac cat gcc tat        340
Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His Ala Tyr
90                  95                  100                 105

agc aac tac aca tgg gtt gac gac act gtg ggc ttc atc atc cat tca        388
Ser Asn Tyr Thr Trp Val Asp Asp Thr Val Gly Phe Ile Ile His Ser
                110                 115                 120

ttt ctc ctc acc ccg tat ttc tct tgg aaa tac agt cac cgg aat cac        436
Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His
                125                 130                 135

cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att ccg aaa        484
His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys
            140                 145                 150

agc aag tcc aaa ctc aag cgt atc tat aaa ctt ctt aac aac cca cct        532
Ser Lys Ser Lys Leu Lys Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro
        155                 160                 165

ggt cga ctg ttg gtt ttg gtt atc atg ttc acc cta gga ttt cct tta        580
Gly Arg Leu Leu Val Leu Val Ile Met Phe Thr Leu Gly Phe Pro Leu
170                 175                 180                 185

tac ctc ttg aca aat att tcc ggc aag aaa tac gat agg ttt gcc aac        628
Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn
                190                 195                 200

cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg ttt cag        676
His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln
                205                 210                 215

gtc ttc ctt tcg gat ctt ggt ctt ctt gct gtg ttt tat gga att aaa        724
Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys
            220                 225                 230

gtt gct gta gca aat aaa gga gct gct tgg gtg gcg tgc atg tat gga        772
Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met Tyr Gly
        235                 240                 245

gtt ccg gtg cta ggc gta ttt acc ttt ttc gat gtg atc acg ttc tta        820
Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr Phe Leu
250                 255                 260                 265
```

```
cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa tgg aac          868
His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu Trp Asn
                270                 275                 280

tgg atc aga ggg gct ttg tca gca atc gat agn gac ttt ggg ttc ctg          916
Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Xaa Asp Phe Gly Phe Leu
                285                 290                 295

aat agt gtt ttc cat gat gtn aca cac act cac gtc atg cat cat ttg          964
Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His His Leu
                300                 305                 310

ttt tca tac att cca cac tat cat gca aag gaa gca agg gat gca atc         1012
Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile
            315                 320                 325

aaa ccg atc ttg ggc gac ttt tat atg atc gat agg act cca att tta        1060
Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu
330                 335                 340                 345

aaa gca atg tgg aga gag ggc agg gaa tgc atg tac atc gag cct gat        1108
Lys Ala Met Trp Arg Glu Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp
                350                 355                 360

agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg tga tcatatgcaa         1157
Ser Lys Leu Lys Gly Val Tyr Trp Tyr His Lys Leu
                365                 370

aatgcacatg cattttcaaa ccctctagtt acctttgttc tatgtataat aagaccgccg      1217

gtcctatggt tttctatgcc taagccaggc gaaatagtta aataatatcg gtatgatgta      1277

atgaaagtat gtggttgtct aaaaaaaaaa aa                                     1309
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<210> 4

<211> 373

<212> PRT

<213> Crepis sp.

<220>

<221> misc_feature

<222> (292)..(292)

<223> The 'Xaa' at location 292 stands for Arg, or Ser.

<220>

<221> misc_feature

<222>   (937)..(937)

<223>   N is any nucleotide residue

<220>

<221>   misc_feature

<222>   (901)..(901)

<223>   N is any nucleotide residue

<400>   4

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Met Gly Ala Gly Gly Arg Gly Arg Ser Glu Lys Ser Val Met Glu Arg
1               5                   10                  15

Val Ser Val Asp Pro Val Thr Phe Ser Leu Ser Asp Leu Lys Gln Ala
                20                  25                  30

Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr Tyr
            35                  40                  45

Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala Asn
        50                  55                  60

Thr Tyr Ile Pro Asn Leu Pro His Pro Leu Ala Tyr Leu Ala Trp Pro
65                  70                  75                  80

Leu Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile Leu
                85                  90                  95

Gly His Glu Cys Gly His His Ala Tyr Ser Asn Tyr Thr Trp Val Asp
            100                 105                 110

Asp Thr Val Gly Phe Ile Ile His Ser Phe Leu Leu Thr Pro Tyr Phe
        115                 120                 125

Ser Trp Lys Tyr Ser His Arg Asn His His Ser Asn Thr Ser Ser Ile
    130                 135                 140

Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Lys Arg
145                 150                 155                 160

Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu Val
                165                 170                 175
```

Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile Ser
         180   185   190

Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro
         195   200   205

Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu Gly
         210   215   220

Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys Gly
225   230   235   240

Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val Phe
         245   250   255

Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser Ser
         260   265   270

Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu Ser
         275   280   285

Ala Ile Asp Xaa Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp Val
         290   295   300

Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His Tyr
305   310   315   320

His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp Phe
         325   330   335

Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu Gly
         340   345   350

Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val Tyr
         355   360   365

Trp Tyr His Lys Leu
         370

<210> 5

<211> 550

<212> DNA

<213> Vernonia galamensis

<220>

<221> CDS

<222> (1)..(549)

<223>

<400> 5
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cat cac gcc ttc agt gac tat caa tgg ata gac gac act gtg ggc ttc      48
His His Ala Phe Ser Asp Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe
1               5                   10                  15

atc ctt cac ttt gca ctc ttc acc cct tat ttc tct tgg aaa tac agt      96
Ile Leu His Phe Ala Leu Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser
                20                  25                  30

cac cgt aat cac cat gcc aac aca aac tct ctt gta acc gat gaa gta     144
His Arg Asn His His Ala Asn Thr Asn Ser Leu Val Thr Asp Glu Val
        35                  40                  45

tac atc cct aaa gtt aaa tcc aag gtc aag att tat tcc aaa atc ctt     192
Tyr Ile Pro Lys Val Lys Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu
    50                  55                  60

aac aac cct cct ggt cgc gtt ttc acc ttg gct ttc aga ttg atc gtg     240
Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Ala Phe Arg Leu Ile Val
65                  70                  75                  80

ggt ttt cct tta tac ctt ttc acc aat gtt tca ggc aag aaa tac gaa     288
Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu
                85                  90                  95

cgt ttt gcc aac cat ttt gat ccc atg agt ccc att ttc acc gag cgt     336
Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Thr Glu Arg
                100                 105                 110

gag cat gta caa gtc ttg ctt tct gat ttt ggt ctc ata gca gtt gct     384
Glu His Val Gln Val Leu Leu Ser Asp Phe Gly Leu Ile Ala Val Ala
        115                 120                 125

tac gtg gtt cgt caa gct gta ctg gct aaa gga ggt gct tgg gtg atg     432
Tyr Val Val Arg Gln Ala Val Leu Ala Lys Gly Gly Ala Trp Val Met
    130                 135                 140

tgc att tac gga gtt cct gtg ctg gcc gta aac gca ttc ttt gtt tta     480
Cys Ile Tyr Gly Val Pro Val Leu Ala Val Asn Ala Phe Phe Val Leu
145                 150                 155                 160
```

```
atc act tat ctt cac cac acg cat ctc tca ctg ccc cac tat gat agc          528
Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr Asp Ser
                165             170             175

tca gaa tgg gac tgg cta cga g                                            550
Ser Glu Trp Asp Trp Leu Arg
                180
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<210> 6

<211> 183

<212> PRT

<213> Vernonia galamensis

<400> 6

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His His Ala Phe Ser Asp Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe
1               5                   10              15


Ile Leu His Phe Ala Leu Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser
                20              25              30


His Arg Asn His His Ala Asn Thr Asn Ser Leu Val Thr Asp Glu Val
            35              40              45


Tyr Ile Pro Lys Val Lys Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu
        50              55              60


Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Ala Phe Arg Leu Ile Val
65              70              75              80


Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu
                85              90              95


Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Thr Glu Arg
                100             105             110


Glu His Val Gln Val Leu Leu Ser Asp Phe Gly Leu Ile Ala Val Ala
        115             120             125


Tyr Val Val Arg Gln Ala Val Leu Ala Lys Gly Gly Ala Trp Val Met
        130             135             140


Cys Ile Tyr Gly Val Pro Val Leu Ala Val Asn Ala Phe Phe Val Leu
145             150             155             160
```

```
Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr Asp Ser
                165                 170                 175

Ser Glu Trp Asp Trp Leu Arg
            180
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<210> 7

<211> 177

<212> DNA

<213> Crepis alpina

<220>

<221> CDS

<222> (1)..(177)

<223>

<400> 7

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gaa tgc ggt cac cat gcc ttc agc gac tac cag tgg gtt gac gac aat      48
Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Asn
1               5                   10                  15

gtg ggc ttc atc ctc cac tcg ttt ctc atg acc ccg tat ttc tcc tgg      96
Val Gly Phe Ile Leu His Ser Phe Leu Met Thr Pro Tyr Phe Ser Trp
                20                  25                  30

aaa tac agc cac cgg aac cac cat gcc aac aca aat tcg ctt gac aac      144
Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn
                35                  40                  45

gat gaa gtt tac atc ccc aaa agc aag gcc aaa                          177
Asp Glu Val Tyr Ile Pro Lys Ser Lys Ala Lys
    50                  55
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<210> 8

<211> 59

<212> PRT

<213> Crepis alpina

<400> 8

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Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Asn
1               5                   10                  15
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Val Gly Phe Ile Leu His Ser Phe Leu Met Thr Pro Tyr Phe Ser Trp
            20   25   30

Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn
            35   40   45

Asp Glu Val Tyr Ile Pro Lys Ser Lys Ala Lys
        50   55

<210> 9

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 9

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
1   5   10   15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
            20   25   30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
            35   40   45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
        50   55   60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65   70   75   80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
                85   90   95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
                100   105   110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
            115   120   125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
    130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                165   170   175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
            180   185   190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
        195   200   205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
    210   215   220

Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
225   230   235   240

Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
            245   250   255

Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
            260   265   270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
    275   280   285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
    290   295   300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
305   310   315   320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
            325   330   335

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
            340   345   350

Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
    355   360   365

Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
    370   375   380

<210> 10

<211> 384

<212> PRT

<213> Brassica juncea

<400> 10

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Ser Pro Lys Lys Ser
1   5   10   15

Glu Thr Asp Thr Leu Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
         20   25   30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
         35   40   45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Val Ala Ser
    50   55   60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
65   70   75   80

Leu Ser Tyr Val Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Val Val
         85   90   95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
         100   105   110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
         115   120   125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
         130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
            165   170   175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
            180   185   190

Tyr Trp Ala Phe Asn Val Ser Gly Arg Pro Tyr Pro Glu Gly Phe Ala
            195   200   205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
            210   215   220

Gln Ile Tyr Val Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
225   230   235   240

Tyr Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Leu Tyr
            245   250   255

Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr
            260   265   270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
            275   280   285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
            290   295   300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305   310   315   320

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Val Thr Lys Ala
            325   330   335

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp
            340   345   350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
            355   360   365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
            370   375   380

<210> 11

<211> 367

<212> PRT

<213> Glycine max

<400> 11

Met Gly Ala Gly Gly Arg Thr Asp Val Pro Pro Ala Asn Arg Lys Ser
1   5   10   15

Glu Val Asp Pro Leu Lys Arg Val Pro Phe Glu Lys Pro Gln Phe Ser
            20   25   30

Leu Ser Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
            35   40   45

Val Leu Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe
        50   55   60

Cys Leu Tyr Tyr Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro
65   70   75   80

Leu Ser Phe Arg Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile
                85   90   95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
                100   105   110

Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly Leu Ile Leu His Ser
            115   120   125

Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
        130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Gly Arg Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu
                165   170   175

Tyr Leu Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
         180   185   190

His Tyr Asp Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
         195   200   205

Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Val Tyr Gly Leu Phe
         210   215   220

Arg Leu Ala Met Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly
225   230   235   240

Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Phe Leu
            245   250   255

Gln His Thr His Pro Ala Leu Pro His Tyr Thr Ser Ser Glu Trp Asp
         260   265   270

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
         275   280   285

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
     290   295   300

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
305   310   315   320

Lys Pro Ile Leu Gly Glu Tyr Tyr Arg Phe Asp Glu Thr Pro Phe Val
            325   330   335

Lys Ala Met Trp Arg Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro Asp
         340   345   350

Gln Ser Thr Glu Ser Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
        355   360   365

<210> 12

<211> 383

<212> PRT

<213> Solanum commersonii

<400> 12

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Met Gly Ala Gly Gly Arg Met Ser Ala Pro Asn Gly Glu Thr Glu Val
1               5               10              15


Lys Arg Asn Pro Leu Gln Lys Val Pro Thr Ser Lys Pro Pro Phe Thr
            20              25              30


Val Gly Asp Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
        35              40              45


Leu Ile Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Ile Leu Val Ser
        50              55              60


Ile Met Tyr Tyr Val Ala Asn Thr Tyr Phe His Leu Leu Pro Ser Pro
65              70              75              80


Tyr Cys Tyr Ile Ala Trp Pro Ile Tyr Trp Ile Cys Gln Gly Cys Val
                85              90              95


Cys Thr Gly Ile Trp Val Asn Ala His Glu Cys Gly His His Ala Phe
            100             105             110


Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
            115             120             125


Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
        130             135             140


His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145             150             155             160


Pro Lys Ser Gln Leu Gly Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro
            165             170             175


Gly Arg Val Leu Ser Leu Thr Ile Thr Leu Thr Leu Gly Trp Pro Leu
            180             185             190


Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
            195             200             205


His Tyr Asp Pro Tyr Gly Pro Ile Tyr Asn Asn Arg Glu Arg Leu Gln
        210             215             220
```

Ile Phe Ile Ser Asp Ala Gly Val Leu Gly Val Cys Tyr Leu Leu Tyr
225   230   235   240

Arg Ile Ala Leu Val Lys Gly Leu Ala Trp Leu Val Cys Val Tyr Gly
            245   250   255

Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
            260   265   270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asp
        275   280   285

Trp Leu Arg Gly Ala Leu Ala Thr Cys Asp Arg Asp Tyr Gly Val Leu
        290   295   300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Val His His Leu
305   310   315   320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Val
            325   330   335

Lys Pro Leu Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Ile Tyr
            340   345   350

Lys Glu Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Lys Asp
        355   360   365

Glu Ser Ser Gln Gly Lys Gly Val Phe Trp Tyr Lys Asn Lys Leu
    370   375   380

<210> 13

<211> 387

<212> PRT

<213> Glycine max

<400> 13

Met Gly Leu Ala Lys Glu Thr Thr Met Gly Gly Arg Gly Arg Val Ala
1   5   10   15

Lys Val Glu Val Gln Gly Lys Lys Pro Leu Ser Arg Val Pro Asn Thr
          20   25   30

Lys Pro Pro Phe Thr Val Gly Gln Leu Lys Lys Ala Ile Pro Pro His
          35   40   45

Cys Phe Gln Arg Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp
    50   55   60

Leu Ser Phe Ala Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu
65   70   75   80

Leu Pro Gln Pro Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu
              85   90   95

Gln Gly Cys Leu Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly
          100   105   110

His His Ala Phe Ser Lys Tyr Gln Trp Val Asp Asp Val Val Gly Leu
          115   120   125

Thr Leu His Ser Thr Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser
          130   135   140

His Arg Arg His His Ser Asn Thr Gly Ser Leu Asp Arg Asp Glu Val
145   150   155   160

Phe Val Pro Lys Pro Lys Ser Lys Val Ala Trp Phe Ser Lys Tyr Leu
              165   170   175

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
          180   185   190

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
          195   200   205

Ser Phe Ala Ser His Tyr His Pro Tyr Ala Pro Ile Tyr Ser Asn Arg
    210   215   220

Glu Arg Leu Leu Ile Tyr Val Ser Asp Val Ala Leu Phe Ser Val Thr
225   230   235   240

Tyr Ser Leu Tyr Arg Val Ala Thr Leu Lys Gly Leu Val Trp Leu Leu
             245   250   255

Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Thr
            260   265   270

Ile Thr Tyr Leu Gln His Thr His Phe Ala Leu Pro His Tyr Asp Ser
         275   280   285

Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr Met Asp Arg Asp
     290   295   300

Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr Asp Thr His Val
305   310   315   320

Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
            325   330   335

Thr Asn Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp
            340   345   350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr
         355   360   365

Val Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg
     370   375   380

Asn Lys Tyr
385

<210> 14

<211> 387

<212> PRT

<213> Ricinus communis

<400> 14

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
1   5   10   15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
            20   25   30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
      35   40   45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
      50   55   60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
65   70   75   80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
          85   90   95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
          100   105   110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
          115   120   125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
          130   135   140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
145   150   155   160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
          165   170   175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
          180   185   190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
          195   200   205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
          210   215   220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
225   230   235   240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
          245   250   255

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Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
            260             265             270


Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
            275             280             285


Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
            290             295             300


Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
305             310             315             320


Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
            325             330             335


Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
            340             345             350


Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
            355             360             365


Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
    370             375             380


Asn Lys Tyr
385


<210>  15

<211>  6

<212>  PRT

<213>  mixed function monooxygenase peptide motif


<400>  15

His Glu Cys Gly His His
1                 5

<210>  16

<211>  5

<212>  PRT
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<213> mixed function monooxygenase peptide motif

<400> 16

His Arg Asn His His
1   5

<210> 17

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 17

His Val Met His His
1   5

<210> 18

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 18

His Val Leu His His
1   5

<210> 19

<211> 1199

<212> DNA

<213> Vernonia galamensis

<220>

<221> CDS

<222> (44)..(1195)

<223>

<400> 19

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tattacacat ttacactgat ctgttaatca aatttcaaac aaa atg gga gct ggt        55
                                                    Met Gly Ala Gly
                                                    1

ggc cga atg aat acc acc gat gat gat cag aag aat ctc ttc caa cgc       103
Gly Arg Met Asn Thr Thr Asp Asp Asp Gln Lys Asn Leu Phe Gln Arg
5               10              15                      20

gta cca gcc tcc aaa cca cca ttc tcc ttg gct gat ctt aag aaa gcc       151
Val Pro Ala Ser Lys Pro Pro Phe Ser Leu Ala Asp Leu Lys Lys Ala
                25              30              35

ata cca ccc cac tgt ttc caa aga tcc ctc ctc cgt tca tct tac tat       199
Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Arg Ser Ser Tyr Tyr
            40              45              50

gtg gtt cat gat ctc gtc gta gcc tac gtc ttt tac tat ctc gcc aac       247
Val Val His Asp Leu Val Val Ala Tyr Val Phe Tyr Tyr Leu Ala Asn
            55              60              65

aca tac atc cct ctt ctt ccc tcc cct ctt gcc tac tta tta gct tgg       295
Thr Tyr Ile Pro Leu Leu Pro Ser Pro Leu Ala Tyr Leu Leu Ala Trp
    70              75              80

ccc ctt tac tgg ttc tgt cag ggt agc atc ctc acc ggt gtc tgg gtc       343
Pro Leu Tyr Trp Phe Cys Gln Gly Ser Ile Leu Thr Gly Val Trp Val
85              90              95                      100

atc ggt cat gaa tgt ggc cac cat gcc ttc agt gac tat caa tgg ata       391
Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Ile
                105             110             115

gac gac act gtg ggc ttc atc ctt cac tct gca ctc ttc acc cct tat       439
Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Phe Thr Pro Tyr
            120             125             130

ttc tct tgg aaa tac agt cac cgt aat cac cat gcc aac aca aac tct       487
Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser
    135             140             145

ctt gat aac gat gaa gta tac atc cct aaa gtt aaa tcc aag gtc aag       535
Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Val Lys Ser Lys Val Lys
    150             155             160

att tat tcc aaa atc ctt aac aac cct cct ggt cgc gtt ttc acc ttg       583
Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr Leu
165             170             175             180

gct ttc aga ttg atc gtg ggt ttt cct tta tac ctt ttc acc aat gtt       631
Ala Phe Arg Leu Ile Val Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val
            185             190             195

tca ggc aag aaa tac gaa cgt ttt gcc aac cat ttt gat ccc atg agt       679
Ser Gly Lys Lys Tyr Glu Arg Phe Ala Asn His Phe Asp Pro Met Ser
            200             205             210
```

```
ccc att ttc acc gag cgt gag cat gta caa gtc ttg ctt tct gat ttt        727
Pro Ile Phe Thr Glu Arg Glu His Val Gln Val Leu Leu Ser Asp Phe
        215             220             225

ggt ctc ata gca gtt gct tac gtg gtt cgt caa gct gta ctg gct aaa        775
Gly Leu Ile Ala Val Ala Tyr Val Val Arg Gln Ala Val Leu Ala Lys
    230             235             240

gga ggt gct tgg gtg atg tgc att tac gga gtt cct gtg ctg gcc gta        823
Gly Gly Ala Trp Val Met Cys Ile Tyr Gly Val Pro Val Leu Ala Val
245             250             255             260

aac gca ttc ttt gtt tta atc act tat ctt cac cac acg cat ctc tca        871
Asn Ala Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu Ser
                265             270             275

ctg cct cac tat gat tcg act gaa tgg gac tgg atc aag gga gct ttg        919
Leu Pro His Tyr Asp Ser Thr Glu Trp Asp Trp Ile Lys Gly Ala Leu
                280             285             290

tgc acc atc gac aga gat ttc gga ttc ttg aat agg gtt ttc cac gac        967
Cys Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His Asp
        295             300             305

gtg aca cac acc cat gtg ttg cat cat ttg ata tcg tac att cct cat        1015
Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro His
    310             315             320

tat cat gca aag gag gca aga gac gcc atc aaa ccg gtg ttg ggc gaa        1063
Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly Glu
325             330             335             340

tac tat aag atc gac agg aca ccg atc gtg aag gca atg tgg agg gaa        1111
Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Val Lys Ala Met Trp Arg Glu
                345             350             355

gca aag aat gca tat aca ttg agg ctg atg aag ata gcg agc acc aag        1159
Ala Lys Asn Ala Tyr Thr Leu Arg Leu Met Lys Ile Ala Ser Thr Lys
                360             365             370

gca cat act ggt acc aca agt tgt aaa gcc aga tcc taag                   1199
Ala His Thr Gly Thr Thr Ser Cys Lys Ala Arg Ser
        375             380
```

<210> 20

<211> 384

<212> PRT

<213> Vernonia galamensis

<400> 20

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Met Gly Ala Gly Gly Arg Met Asn Thr Thr Asp Asp Asp Gln Lys Asn
1             5                 10              15

Leu Phe Gln Arg Val Pro Ala Ser Lys Pro Pro Phe Ser Leu Ala Asp
            20              25              30

Leu Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Arg
        35              40              45

Ser Ser Tyr Tyr Val Val His Asp Leu Val Val Ala Tyr Val Phe Tyr
    50              55              60

Tyr Leu Ala Asn Thr Tyr Ile Pro Leu Leu Pro Ser Pro Leu Ala Tyr
65              70              75              80

Leu Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Gly Ser Ile Leu Thr
            85              90              95

Gly Val Trp Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp
            100             105             110

Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu
        115             120             125

Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala
    130             135             140

Asn Thr Asn Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Val Lys
145             150             155             160

Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg
            165             170             175

Val Phe Thr Leu Ala Phe Arg Leu Ile Val Gly Phe Pro Leu Tyr Leu
            180             185             190

Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu Arg Phe Ala Asn His Phe
        195             200             205

Asp Pro Met Ser Pro Ile Phe Thr Glu Arg Glu His Val Gln Val Leu
210             215             220
```

```
Leu Ser Asp Phe Gly Leu Ile Ala Val Ala Tyr Val Val Arg Gln Ala
225             230         235             240


Val Leu Ala Lys Gly Gly Ala Trp Val Met Cys Ile Tyr Gly Val Pro
            245             250             255


Val Leu Ala Val Asn Ala Phe Phe Val Leu Ile Thr Tyr Leu His His
            260             265             270


Thr His Leu Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asp Trp Ile
            275             280         285


Lys Gly Ala Leu Cys Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg
            290             295             300


Val Phe His Asp Val Thr His Thr His Val Leu His His Leu Ile Ser
305             310             315             320


Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro
                325             330             335


Val Leu Gly Glu Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Val Lys Ala
            340             345             350


Met Trp Arg Glu Ala Lys Asn Ala Tyr Thr Leu Arg Leu Met Lys Ile
            355             360             365


Ala Ser Thr Lys Ala His Thr Gly Thr Thr Ser Cys Lys Ala Arg Ser
    370             375             380
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<210> 21

<211> 5

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(4)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any amino acid; Xaa at position 4 is any amino acid;

```
<400>   21

His Xaa Xaa Xaa His
1               5


<210>   22

<211>   6

<212>   PRT

<213>   mixed function monooxygenase consensus motif


<220>

<221>   MISC_FEATURE

<222>   (2)..(5)

<223>   Xaa at position 2 is any amino acid; Xaa at position 3 is any ami
        no acid; Xaa at position 4 is any amino acid;Xaa at position 5 is
         any amino acid;


<400>   22

His Xaa Xaa Xaa Xaa His
1               5


<210>   23

<211>   5

<212>   PRT

<213>   mixed function monooxygenase consensus motif


<220>

<221>   MISC_FEATURE

<222>   (2)..(3)

<223>   Xaa at position 2 is any amino acid; Xaa at position 3 is any ami
        no acid;


<400>   23

His Xaa Xaa His His
1               5
```

<210> 24

<211> 6

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(4)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any ami
      no acid; Xaa at position 4 is any amino acid;

<400> 24

His Xaa Xaa Xaa His His
1   5